

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2006, 17:51:08 ; Search time 3466.43 Seconds
(without alignments)
10607.392 Million cell updates/sec

Title: US-10-698-160-1

Perfect score: 575

Sequence: 1 tcaggccagtgctcaggag.....gcgaaagggtggtggctgt 575

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_env.*

2: gb_pat.*

3: gb_ph.*

4: gb_pl.*

5: gb_pr.*

6: gb_ro.*

7: gb_sts.*

8: gb_sy.*

9: gb_un.*

10: gb_vi.*

11: gb_ov.*

12: gb_hcg.*

13: gb_in.*

14: gb_on.*

15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	575	100.0	171823	10	HV507799 Human her
2	575	100.0	172281	10	EV
3	575	100.0	184113	10	HS4B958RAJ
4	536.6	93.3	3060	10	HS4LMP
5	504.6	87.8	171657	10	HS4LMP1
6	498.2	86.6	2038	10	HS4LMP1
7	498.2	86.6	2038	10	HS4LMP1
8	484.2	84.2	3407	10	HS4LMP1
9	464.8	80.8	1009	10	HU86104
10	451.2	78.5	2031	10	HS4LMP1
11	451.2	78.5	2031	10	HS4LMP1
12	428	74.4	515	10	HHE278797
13	428	74.4	515	10	HHE278798
14	405.6	70.5	515	10	HHE278794
15	405.6	70.5	515	10	HHE278795
16	404	70.3	515	10	HHE278796
17	368.8	64.1	406	10	EBAJ1676
18	202.4	35.2	204	10	EBVLM228

19	200.8	34.9	204	10	EBVLM229
20	199.2	34.6	204	10	EBVLM226
21	199.2	34.6	204	10	EBVLM227
22	199.2	34.6	204	10	EBVLM230
23	185.4	32.2	1397	10	HS4LMPA
24	101	17.6	497	10	SS0728
25	95	16.5	2400	10	HEB08278
26	89.4	15.5	1422	10	HEB08278
27	89.4	15.5	1422	10	HEB08278
28	86.4	15.0	7218	2	I66494
29	81.6	14.2	38128	12	BX296528
30	81.2	14.1	205691	12	AC087227
31	81	14.1	265985	12	AC087226
32	80.8	14.1	56970	12	AC138096
33	80.2	13.9	497	10	S69600
34	78.6	13.7	303091	12	AC084799
35	77.4	13.5	252689	12	AC079433
36	75.6	13.1	80133	12	AC021347
37	75	13.0	209887	12	AC079424
38	74.8	13.0	235310	12	AC094274
39	74.4	12.9	222707	12	AC079425
40	74.2	12.9	2431	10	AY519199
41	74	12.9	122272	12	AC143808
42	74	12.9	134940	12	AC018939
43	74	12.9	185822	12	AC073554
44	74	12.9	253711	12	AC143908
45	73.6	12.8	143733	12	AC142786

ALIGNMENTS

RESULT 1	HHV507799	Human herpesvirus 4 complete wild type genome.	171823 bp	DNA	circular VRL 31-JAN-2006
LOCUS	HHV507799	Human herpesvirus 4 complete wild type genome.	171823 bp	DNA	circular VRL 31-JAN-2006
DEFINITION	HHV507799	Human herpesvirus 4 complete wild type genome.	171823 bp	DNA	circular VRL 31-JAN-2006
ACCESSION	HHV507799	Human herpesvirus 4 complete wild type genome.	171823 bp	DNA	circular VRL 31-JAN-2006
VERSION	HHV507799.2	GI:86261677			
KEYWORDS	complete genome.				
SOURCE	Human herpesvirus 4 (Epstein-Barr virus)				
ORGANISM	Human herpesvirus 4				
REFERENCE	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.				
AUTHORS	Arrand, J.R., Rymo, L., Walsh, J.E., Bjorck, E., Lindahl, T. and Griffin, B.E.				
TITLE	Molecular cloning of the complete Epstein-Barr virus genome as a set of overlapping restriction endonuclease fragments				
JOURNAL	Nucleic Acids Res. 9 (13), 2999-3014 (1981)				
PUBMED	6269068				
REFERENCE	2				
AUTHORS	Kozak, M.				
TITLE	Possible role of flanking nucleotides in recognition of the AUG initiator codon by eukaryotic ribosomes				
JOURNAL	Nucleic Acids Res. 9 (20), 5233-5252 (1981)				
PUBMED	7301588				
REFERENCE	3				
AUTHORS	Deininger, P.L., Bankier, A., Farrell, P., Baer, R. and Barrell, B.				
TITLE	Sequence analysis and in vitro transcription of portions of the Epstein-Barr virus genome				
JOURNAL	J. Cell. Biochem. 19 (3), 267-274 (1982)				
PUBMED	6296170				
REFERENCE	4				
AUTHORS	Farrell, P.J., Bankier, A., Seguin, C., Deininger, P. and Barrell, B.G.				
TITLE	Latent and lytic cycle promoters of Epstein-Barr virus				
JOURNAL	EMBO J. 2 (8), 1331-1338 (1983)				
PUBMED	10872327				
REFERENCE	5				
AUTHORS	Farrell, P.J., Deininger, P.L., Bankier, A. and Barrell, B.				
TITLE	Homologous upstream sequences near Epstein-Barr virus promoters				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 80 (6), 1565-1569 (1983)				
PUBMED	6300857				
REFERENCE	6				

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OM nucleic - nucleic search, using sw model

Run on: June 6, 2006, 17:26:38 ; Search time 433.304 Seconds
(without alignments)
9252.273 Million cell updates/sec

Title: US-10-698-160-1

Perfect score: 575

Sequence: 1 tcaggcgatgtgtcaggag.....gcgaaagggtgtgggtgtgt 575

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_8.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001as.*
- 5: Geneseq2001bs.*
- 6: Geneseq2002as.*
- 7: Geneseq2002bs.*
- 8: Geneseq2003as.*
- 9: Geneseq2003bs.*
- 10: Geneseq2003cs.*
- 11: Geneseq2003ds.*
- 12: Geneseq2004as.*
- 13: Geneseq2004bs.*
- 14: Geneseq2005s.*
- 15: Geneseq2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	575	100.0	1177	12 ADO43140	Ado43140 Epstein-B
2	575	100.0	172281	12 Adn12161	Adn12161 Epstein-B
C 3	451.2	78.5	2031	12 Adn12158	Adn12158 Epstein-B
C 4	69.2	12.0	1337	2 AAZ17263	Aaz17263 Human gen
5	68.2	11.9	5452	10 ADC86736	Adc86736 Human GPC
6	67.6	11.8	3163	10 ADC87060	Adc87060 Human GPC
7	67.4	11.7	3133	10 ADC86738	Adc86738 Human GPC
8	66.8	11.6	629	13 ACN54594	Acn54594 Cotton an
9	66.8	11.6	12733	6 ABK98631	Abk98631 Vector pE
10	66.8	11.6	12733	9 ACD13882	Acd13882 L. lactis
11	66.8	11.6	12739	6 ABK98592	Abk98592 Vector pE
12	66.8	11.6	12739	9 ACD13843	Acd13843 Plasmid p
13	63.6	11.1	588	13 ACN54596	Acn54596 Cotton an
14	63.6	11.1	1117	10 ADC86688	Adc86688 Human GPC
C 15	62.6	10.9	1065	6 ABT09682	Abt09682 Human PAL
16	62	10.8	1000	3 AAA02484	Aaa02484 Human col
C 17	61.6	10.7	28198	10 ADG37080	Adg37080 Mouse pla
C 18	61	10.6	1064	6 ABT09678	Abt09678 Human PAL

C 19	60.6	10.5	500	12 ADP85918	Adp85918 Synthetic
20	59.6	10.4	1416	8 ABZ20967	Abz20967 Animal te
21	59.4	10.3	1218	3 AAA02488	Aaa02488 Human col
C 22	59.2	10.3	600	6 ABQ52497	Abq52497 Oligonuel
23	59.2	10.3	600	6 ABQ52496	Abq52496 Oligonuel
24	58.4	10.2	1593	3 AAA02504	Aaa02504 Human col
C 25	56.8	9.9	32195	4 AAL04180	Aal04180 Human rep
26	55.6	9.7	518	6 ABQ52056	Abq52056 Oligonuel
C 27	55.6	9.7	518	6 ABQ52057	Abq52057 Oligonuel
28	55.4	9.6	1327	6 ABQ68452	Abq68452 Listeria
C 29	55	9.6	100976	14 AEC82936	Aec82936 Breast ca
30	54.4	9.5	53522	6 AAD30228	Aad30228 Human PKD
C 31	54.4	9.5	53522	13 ADU03973	Adu03973 Human pol
C 32	54.4	9.5	53522	14 AEB35216	Aeb35216 Human Gef
C 33	54.4	9.5	53526	2 AAT94101	Aat94101 Human PKD
C 34	54.4	9.5	53577	2 AAT18551	Aat18551 Human pol
C 35	54.4	9.5	53577	2 AAT94108	Aat94108 Human PKD
36	53.4	9.3	931	11 ACN87435	Acn87435 Breast ca
C 37	53.4	9.3	2188	2 AAZ77506	Aaz77506 Human ova
C 38	53.2	9.3	478	13 ACN51281	Acn51281 Cotton an
C 39	53.2	9.3	1131	12 ADQ23807	Adq23807 Human sof
40	53	9.2	840	6 ABO35494	Abq35494 Oligonuel
C 41	53	9.2	840	6 ABO35495	Abq35495 Oligonuel
C 42	53	9.2	1030	6 ABO42521	Abq42521 Oligonuel
43	53	9.2	1030	6 ABO42520	Abq42520 Oligonuel
44	52.8	9.2	922	10 ADC86708	Adc86708 Human GPC
45	52.6	9.1	1557	14 AEC40130	Aec40130 Porcine e

ALIGNMENTS

RESULT 1
ADO43140
ID ADO43140 standard; DNA; 1177 BP.

XX ADO43140;

XX DT 12-AUG-2004 (first entry)

XX DE Epstein-Barr virus LMP1 gene upstream region.

XX KW Epstein-Barr virus; LMP1; promoter; adenovirus; vector; gene therapy;

XX OS Human herpesvirus 4.

XX FH Key

FT protein_bind Location/Qualifiers

FT /tag= a

FT /bound_moiety= "STAT"

FT /note= "ED-L1 promoter"

FT protein_bind 642..650

FT /tag= b

FT /bound_moiety= "STAT"

FT GC_signal 657..673

FT /tag= c

XX WO2004042025-A2.

XX 21-MAY-2004.

XX 30-OCT-2003; 2003WO-US034858.

XX 01-NOV-2002; 2002US-0423203P.

XX (CELL-) CELL GENESYS INC.

XX PI Yu DC, Ramesh N;

XX WPI; 2004-390609/36.

XX GENBANK; NC_001345.

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OM nucleic - nucleic search, using sw model

Run on: June 6, 2006, 17:52:13 ; Search time 3888.44 Seconds
(without alignments)
8269.032 Million cell updates/sec

Title: US-10-698-160-1
Perfect score: 575
Sequence: 1 tcaggagcagtgtcaggag.....gcgaaagggtgggctgt 575

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues
Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est3:
3: gb_est4:
4: gb_est5:
5: gb_est6:
6: gb_est7:
7: gb_est8:
8: gb_est9:
9: gb_est10:
10: gb_est11:
11: gb_est12:
12: gb_est13:
13: gb_est14:
14: gb_est15:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	85	14.8	1421	9	DN653570 CEC06-C08
2	81.8	14.2	817	9	DN808203 74134031
3	81.8	14.2	1607	10	DV779627 Hw_Fat_35
C 4	81.6	14.2	1129	12	CL045106 CH216-62E
C 5	81.6	14.2	1301	14	AG363665 Mus muscu
C 6	81.6	14.2	1560	12	CL081488 CH216-162
C 7	81.6	14.2	1593	12	CC255263 CH216-42A
C 8	81.4	14.2	1021	3	BQ441712 AGENCOURT
9	81	14.1	1287	13	CW948789 TCB33.1_H
10	80.8	14.1	774	7	BE040676 OF04H04 O
11	80.8	14.1	849	4	CB905469 trico074xk
12	80.8	14.1	849	5	CF876976 trico074xk
13	80.6	14.0	1591	12	CL077232 CH216-143
14	80.6	14.0	1728	12	CG750956 P045-2-H0
15	80.4	14.0	956	13	CW951178 TCB36.3 D
C 16	80.4	14.0	1362	3	BM556092 AGENCOURT
C 17	80.2	13.9	1471	10	DV781271 Hw_Fat_35
C 18	80	13.9	1099	13	CL509275 SATL 811
C 19	80	13.9	1201	12	CL082769 CH216-171

20	80	13.9	1874	14	AG448338	Mus muscu
21	79.8	13.9	932	14	AG134650	Pan trogl
C 22	79.8	13.9	947	4	CA466199	AGENCOURT
23	79.8	13.9	1729	10	DV792917	Hw loin_1
24	79.6	13.8	975	10	DR733207	FGAS07856
25	79.6	13.8	1052	2	BI416480	haap001xa
26	79.6	13.8	1142	4	CB905439	trico074xh
27	79.6	13.8	1142	5	CF876953	trico074xh
28	79.4	13.8	680	14	CR234856	Forward 8
29	79.4	13.8	1040	12	CC281819	CH261-172
30	79.4	13.8	1449	10	DV781216	Hw_Fat_30
31	79.4	13.8	1525	10	DV775320	Hw_Fat_30
C 32	79.2	13.8	805	14	AG513081	Mus muscu
33	79.2	13.8	1013	4	CB905417	trico074xf
34	79.2	13.8	1013	5	CF876937	trico074xf
35	79.2	13.8	1087	4	CB908860	trico086xi
36	79.2	13.8	1087	5	CF882340	trico086xi
37	79.2	13.8	1435	10	DV775155	Hw_Fat_36
38	79.2	13.8	1487	10	DV794756	Hw loin_2
39	79	13.7	666	14	AG080429	Pan trogl
40	79	13.7	1320	10	DV776929	Hw_Fat_35
41	79	13.7	1335	10	DT980579	CLJ189-E0
42	79	13.7	1578	14	AG448781	Mus muscu
C 43	79	13.7	1598	12	CL078355	CH216-149
44	79	13.7	1793	12	CG754612	P050-1-D0
45	78.8	13.7	1183	9	DN710897	CLJ92-A06

ALIGNMENTS

RESULT 1
DN653570
LOCUS
DEFINITION
CEC06-C08.xld-t SHGC-CEC Gasterosteus aculeatus cDNA clone
CEC06-C08 3', mRNA sequence.
DN653570.1 GI:61958819
EST.
Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.
1 (bases 1 to 1421)
Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M.,
Schmutz, J. and Myers, R.M.
Expressed sequence tags from Gasterosteus aculeatus
Unpublished (2003)
Contact: Grimwood, Jane
Stanford Human Genome Center
Stanford University School of Medicine
975 S California Ave, Palo Alto, CA 94304, USA
Tel: 650 320 5917
Fax: 650 320 5801
Email: jane@hgsc.stanford.edu
Plate: 06
High quality sequence start: 4
High quality sequence stop: 347.
Location/Qualifiers
1..1421
/organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/strain="Conner Creek sticklebacks, WA USA"
/db_xref="taxon:69293"
/clone="CEC06-C08"
/sex="mixed male and female"
/tissue_type="skin"
/dev_stage="adult"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="SHGC-CEC"
/note="Vector: Express 1; Total and poly A+ RNA was

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OM nucleic - nucleic search, using sw model

Run on: June 6, 2006, 18:05:44 ; Search time 153.504 Seconds
(without alignments)
7008.836 Million cell updates/sec

Title: US-10-698-160-1
Perfect score: 575
Sequence: 1 tcaggcagtggtcaggag.....gcgaaagggtgtgggtgt 575

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA*

- 1: /EMC_Celerra_IDS33/ptodata/2/ina/1 COMB.seq*
- 2: /EMC_Celerra_IDS33/ptodata/2/ina/5 COMB.seq*
- 3: /EMC_Celerra_IDS33/ptodata/2/ina/6A COMB.seq*
- 4: /EMC_Celerra_IDS33/ptodata/2/ina/6B COMB.seq*
- 5: /EMC_Celerra_IDS33/ptodata/2/ina/7 COMB.seq*
- 6: /EMC_Celerra_IDS33/ptodata/2/ina/H COMB.seq*
- 7: /EMC_Celerra_IDS33/ptodata/2/ina/PCTUS COMB.seq*
- 8: /EMC_Celerra_IDS33/ptodata/2/ina/PP COMB.seq*
- 9: /EMC_Celerra_IDS33/ptodata/2/ina/RE COMB.seq*
- 10: /EMC_Celerra_IDS33/ptodata/2/ina/backfile1.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	86.4	15.0	7218	2	US-08-232-463-14
C 2	69.2	12.0	1337	4	US-09-297-648-4735
C 3	54.4	9.5	53526	3	US-08-658-136-2
C 4	54.4	9.5	53577	3	US-08-658-136-1
C 5	54.4	9.5	53577	3	US-08-460-215A-1
C 6	53.4	9.3	9293	3	US-09-949-016-16801
C 7	53.4	9.3	767677	3	US-09-949-016-12147
C 8	53.4	9.3	767677	3	US-09-949-016-17361
C 9	52.8	9.2	18955	3	US-09-949-016-13343
C 10	52.8	9.2	30678	3	US-09-949-016-12818
C 11	52	9.0	320	3	US-09-165-264-11
C 12	51.8	9.0	1454	4	US-09-297-648-4508
C 13	51.2	8.9	320	3	US-09-165-264-14
C 14	50	8.7	50	2	US-08-171-389-558
C 15	50	8.7	50	2	US-08-123-936-558
C 16	50	8.7	50	2	US-08-475-228A-558
C 17	50	8.7	50	3	US-08-483-080A-558
C 18	50	8.7	50	3	US-09-354-947-558
C 19	50	8.7	50	3	US-09-993-346-558
C 20	50	8.7	50	7	PCT-US933-12388-558
C 21	49.8	8.7	289	3	US-09-007-005-17
C 22	49.8	8.7	289	3	US-09-244-796-17
C 23	49.8	8.7	320	3	US-09-165-264-13

C 24	49.8	8.7	37155	3	US-09-949-016-16945
C 25	49.6	8.6	319	3	US-09-165-264-8
C 26	49.2	8.6	318	3	US-09-165-264-12
C 27	48.6	8.5	320	3	US-09-165-264-7
C 28	48.6	8.5	4897	10	5196516-7
C 29	48	8.3	10968	3	US-09-867-753-3
C 30	47.8	8.3	865	3	US-09-270-767-11042
C 31	47	8.2	12907	3	US-09-949-016-16565
C 32	47	8.2	17977	3	US-09-949-016-12403
C 33	47	8.2	119032	3	US-09-949-016-12160
C 34	47	8.2	119032	3	US-09-949-016-17268
C 35	47	8.2	152331	3	US-09-128-155-16
C 36	46.2	8.0	1235	4	US-09-297-648-3617
C 37	45.8	8.0	1017	4	US-09-297-648-4529
C 38	45.8	8.0	1359	4	US-09-297-648-4725
C 39	45.6	7.9	1185	4	US-09-297-648-4514
C 40	45.2	7.9	1166	3	US-09-072-596-323
C 41	45.2	7.9	1166	3	US-09-072-967-328
C 42	45.2	7.9	1166	3	US-10-193-002-323
C 43	45.2	7.9	1166	3	US-10-084-843-328
C 44	44.8	7.8	1411	4	US-09-297-648-4415
C 45	43.8	7.6	1309	4	US-09-297-648-4724

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, P.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 INMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:

GenCore version 5.1.9
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM nucleic - nucleic search, using sw model
 Run on: June 6, 2006, 18:14:24 ; Search time 1119.71 Seconds
 (without alignments)
 6310.019 Million cell updates/sec

Title: US-10-698-160-1
 Perfect score: 575
 Sequence: 1 tcaggcagtggtgcaggag.....gagaaagggtggtggtgtgt 575

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 18992170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications NA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	575	100.0	575	8	US-10-698-160-1
c 2	72.4	12.6	891	9	Sequence 1, Appli
c 3	72.2	12.6	925	8	Sequence 146045, A
c 4	70.6	12.3	778	8	US-10-425-115-146045
c 5	69.6	12.1	815	8	Sequence 54839, A
c 6	69.4	12.1	985	9	US-10-424-599-54839
c 7	69.2	12.0	1337	10	US-10-425-115-91623
c 8	68.2	11.9	5452	7	US-10-779-543-5579
c 9	68.2	11.9	5452	7	US-10-017-161-1481
c 10	67.8	11.8	766	9	US-10-292-798-1189
c 11	67.6	11.8	3163	7	US-10-425-115-82176
c 12	67.6	11.8	3163	7	US-10-017-161-1857
c 13	67.4	11.7	3133	7	Sequence 1857, Ap
c 14	67.4	11.7	3133	7	US-10-292-798-1513
c 15	66.8	11.6	629	8	Sequence 1513, Ap
c 16	66.8	11.6	12733	6	Sequence 1483, Ap
c 17	66.8	11.6	12739	6	Sequence 1191, Ap
					Sequence 9375, Ap
					Sequence 47, Appli
					Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-10-698-160-1

; Sequence 1, Application US/10698160
 ; Publication No. US20040171159A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DC Yu
 ; APPLICANT: Nagarajan Ramesh
 ; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTOR
 ; TITLE OF INVENTION: COMPRISING EBV-SPECIFIC PROMOTER
 ; FILE REFERENCE: CELL-023
 ; CURRENT APPLICATION NUMBER: US/10/698,160
 ; CURRENT FILING DATE: 2003-10-30
 ; PRIOR APPLICATION NUMBER: 60/423,203
 ; PRIOR FILING DATE: 2002-11-01
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 575
 ; TYPE: DNA
 ; ORGANISM: Epstein Barr virus
 US-10-698-160-1

Query Match	100.0%	Score 575;	DB 8;	Length 575;
Best Local Similarity	100.0%	Pred. No. 5.1e-163;		
Matches 575;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	TCAGGGCAGTGTGTTCAGGAGCAAGCAGTTCAGGAAAGAGGGGCGAGCAGTGTGAGA	60
Db	1	TCAGGGCAGTGTGTTCAGGAGCAAGCAGTTCAGGAAAGAGGGGCGAGCAGTGTGAGA	60
QY	61	GCCTTATGTAGCGGGCTACGTCAGAGTAACGCGTGTTCCTTGGGATGTAGCCCGGGG	120
Db	61	GCCTTATGTAGCGGGCTACGTCAGAGTAACGCGTGTTCCTTGGGATGTAGCCCGGGG	120
QY	121	GATTTCGGGGTCTGCGGAGCGAGTACGGGTACAGATTTCCCGAAACGCGGTGTGTG	180
Db	121	GATTTCGGGGTCTGCGGAGCGAGTACGGGTACAGATTTCCCGAAACGCGGTGTGTG	180
QY	181	TGTGCATGTAAAGCGGTAGAAAGGGAAGTAGAAAGCGTGTGTGTGTGTAGAAAGCGGT	240

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
C 1	41.4	7.2	1682	6	US-10-953-349-31197	Sequence 31197, A	
C 2	38.8	6.7	38187	6	US-10-857-260-31	Sequence 31, Appl	
C 3	38.4	6.7	128361	6	US-10-505-928-151	Sequence 151, App	
C 4	38	6.6	151830	6	US-10-519-335-37	Sequence 37, Appl	
C 5	37.6	6.5	435	6	US-10-953-349-35785	Sequence 35785, A	
C 6	37	6.4	1214	6	US-10-953-349-34664	Sequence 34664, A	
C 7	35.8	6.2	2244	6	US-11-233-657-1477	Sequence 1477, Ap	
C 8	35.6	6.2	1951	6	US-10-953-349-29733	Sequence 29733, A	
C 9	35.6	6.2	11978	7	US-11-257-851A-63	Sequence 63, Appl	
C 10	35.6	6.2	37476	7	US-11-297-134-28	Sequence 28, Appl	
C 11	35.4	6.2	4004	7	US-11-293-657-590	Sequence 590, App	
C 12	35.2	6.1	3029	7	US-11-233-657-1476	Sequence 1476, Ap	
C 13	35	6.1	945	6	US-10-953-349-23294	Sequence 23294, A	
C 14	34.8	6.1	1116	6	US-10-953-349-25725	Sequence 25725, A	
C 15	34	5.9	1683	6	US-10-953-349-38422	Sequence 38422, A	
C 16	34	5.9	1799	7	US-11-293-657-1885	Sequence 1885, Ap	
C 17	33.8	5.9	464	6	US-10-953-349-25482	Sequence 25482, A	
C 18	33.6	5.8	22118	6	US-11-284-877-16	Sequence 16, Appl	
C 19	33	5.7	1773	6	US-10-953-349-32064	Sequence 32064, A	
C 20	32.8	5.7	2845	7	US-11-293-657-1481	Sequence 1481, Ap	
C 21	32.6	5.7	135	6	US-10-488-619-2301	Sequence 2301, Ap	
C 22	32.6	5.7	686	6	US-10-953-349-37022	Sequence 37022, A	
C 23	32.6	5.7	2114	6	US-10-953-349-32708	Sequence 32708, A	
C 24	32.6	5.7	2537	7	US-11-293-657-2092	Sequence 2092, Ap	
C 25	32.4	5.6	1122	6	US-10-953-349-31614	Sequence 31614, A	

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OM nucleic - nucleic search, using sw model

Run on: June 6, 2006, 17:51:08 ; Search time 3285.57 Seconds
(without alignments)
10607.392 Million cell updates/sec

Title: US-10-698-160-2
Perfect score: 545
Sequence: 1 cgcacaaactggcgcaaatg.....catttcaggcggttttgea 545

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

1: gb_env.*
2: gb_pat.*
3: gb_ph.*
4: gb_pl.*
5: gb_pr.*
6: gb_ro.*
7: gb_sts.*
8: gb_sy.*
9: gb_un.*
10: gb_vi.*
11: gb_ov.*
12: gb_hcg.*
13: gb_in.*
14: gb_om.*
15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	545	100.0	171823	10	HV507799 Human her
2	545	100.0	172281	10	EBV
3	545	100.0	184113	10	H54B958RAJ
4	543.4	99.7	171657	10	AY961628 Human her
5	410.8	75.4	426	10	HHE414532 Human her
6	410.8	75.4	426	10	HHE414533 Human her
7	397.2	72.9	425	10	HHE414534 Human her
8	397.2	72.9	425	10	HHE414535 Human her
9	110.6	20.3	171096	10	AY037858 Cercopith
10	75	13.8	2035	2	CQ850504 Sequence
11	75	13.8	2035	5	AK127652 Homo sapi
12	50.4	9.2	125020	5	AF429315 Homo sapi
13	48	8.8	2026	10	EBVTRM
14	45.4	8.3	50	2	AX930675 Sequence
15	45.4	8.3	50	2	CQ774555 Sequence
16	45.4	8.3	50	2	CQ794832 Sequence
17	45.4	8.3	50	2	CQ881165 Sequence
18	45.4	8.3	50	2	CQ891130 Sequence

19	45.4	8.3	50	2	DD211186	DD211186 Modulator
20	45.4	8.3	50	2	DD211360	DD211360 Medical T
21	45.4	8.3	50	2	AX743545	AX743545 Sequence
22	45.4	8.3	50	2	AX766903	AX766903 Sequence
23	45.4	8.3	50	2	AX774657	AX774657 Sequence
C 24	44	8.1	50	2	DD211187	DD211187 Modulator
C 25	44	8.1	50	2	AX743546	AX743546 Sequence
C 26	44	8.1	50	2	AX766958	AX766958 Sequence
C 27	43.8	8.0	125020	5	AF429315	AF429315 Homo sapi
C 28	41.4	7.6	2000	2	AX655393	AX655393 Sequence
C 29	39.6	7.3	7218	2	I66494	I66494 Sequence 14
C 30	39.6	7.3	170979	5	AC007950	AC007950 Homo sapi
C 31	39.6	7.3	171456	5	AC023591	AC023591 Homo sapi
C 32	38.8	7.1	258174	12	AC079429	AC079429 Mus muscu
C 33	38.6	7.1	156987	12	AC027494	AC027494 Homo sapi
C 34	38.6	7.1	158741	5	AC091905	AC091905 Homo sapi
C 35	38.6	7.1	189592	12	AC019146	AC019146 Homo sapi
C 36	38.4	7.0	3576	5	AK026479	AK026479 Homo sapi
C 37	38	7.0	110000	12	CT005271_13	Continuation (14 o
C 38	38	7.0	110000	15	CP000096_09	Continuation (10 o
C 39	38	7.0	241138	12	AC118496	AC118496 Rattus no
C 40	37.8	6.9	3637	6	AK128964	AK128964 Mus muscu
C 41	37.6	6.9	29074	13	LMFL5213T	AL352992 Leishmani
C 42	37.6	6.9	110000	12	CT005267_08	Continuation (9 of
C 43	37.6	6.9	190427	12	AC119057	AC119057 Papio anu
C 44	37.4	6.9	182116	5	AC093831	AC093831 Homo sapi
C 45	37.2	6.8	165083	6	AC120554	AC120554 Mus muscu

ALIGNMENTS

RESULT 1	HHV507799	171823 bp	DNA	circular VRL 31-JAN-2006
LOCUS	Human herpesvirus 4 complete wild type genome.			
DEFINITION	Human herpesvirus 4 complete wild type genome.			
ACCESSION	AJ507799.2	GI:86261677		
VERSION	complete genome.			
KEYWORDS	Human herpesvirus 4 (Epstein-Barr virus)			
SOURCE	Human herpesvirus 4			
ORGANISM	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.			
REFERENCE	1			
AUTHORS	Arrand, J.R., Rymo, L., Walsh, J.E., Bjorck, E., Lindahl, T. and Griffin, B.E.			
TITLE	Molecular cloning of the complete Epstein-Barr virus genome as a set of overlapping restriction endonuclease fragments			
JOURNAL	Nucleic Acids Res. 9 (13), 2999-3014 (1981)			
PUBMED	6269068			
REFERENCE	2			
AUTHORS	Kozak, M.			
TITLE	Possible role of flanking nucleotides in recognition of the AUG initiator codon by eukaryotic ribosomes			
JOURNAL	Nucleic Acids Res. 9 (20), 5233-5252 (1981)			
PUBMED	7301588			
REFERENCE	3			
AUTHORS	Deininger, P.L., Bankier, A., Farrell, P., Baer, R. and Barrell, B.			
TITLE	Sequence analysis and in vitro transcription of portions of the Epstein-Barr virus genome			
JOURNAL	J. Cell. Biochem. 19 (3), 267-274 (1982)			
PUBMED	6296170			
REFERENCE	4			
AUTHORS	Farrell, P.J., Bankier, A., Seguin, C., Deininger, P. and Barrell, B.G.			
TITLE	Latent and lytic cycle promoters of Epstein-Barr virus			
JOURNAL	EMBO J. 2 (8), 1331-1338 (1983)			
PUBMED	10872327			
REFERENCE	5			
AUTHORS	Farrell, P.J., Deininger, P.L., Bankier, A. and Barrell, B.			
TITLE	Homologous upstream sequences near Epstein-Barr virus promoters			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 80 (6), 1565-1569 (1983)			
PUBMED	6300857			
REFERENCE	6			

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OM nucleic - nucleic search, using sw model

Run on: June 6, 2006, 17:26:38 ; Search time 410.696 Seconds
(without alignments)
9252.273 Million cell updates/sec

Title: US-10-698-160-2

Perfect score: 545

Sequence: 1 cgacacaaactgcgcaaatg.....catttcaggccggttttgcga 545

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq 8:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001as:*

5: Geneseq2001bs:*

6: Geneseq2002as:*

7: Geneseq2002bs:*

8: Geneseq2003as:*

9: Geneseq2003bs:*

10: Geneseq2003cs:*

11: Geneseq2003ds:*

12: Geneseq2004as:*

13: Geneseq2004bs:*

14: Geneseq2005a:*

15: Geneseq2005b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	545	100.0	545	ADO43141	Ado43141 Epstein-B
2	545	100.0	172281	ADN12161	Adn12161 Epstein-B
3	110.6	20.3	171096	ADT05874	Adt05874 Cercopit
4	75	13.8	2035	ADR07467	Adr07467 Full leng
5	45.4	8.3	50	ABZ77478	Abz77478 Oligonuc
6	45.4	8.3	50	ACC83339	Acc83339 TPI promo
7	45.4	8.3	50	ABZ81622	Abz81622 TPI promo
8	45.4	8.3	50	ACC84643	Acc84643 TPI promo
9	45.4	8.3	50	ACC78948	Acc78948 TPI promo
10	45.4	8.3	50	ACF58279	Acf58279 Oligo use
11	45.4	8.3	50	ADH39824	Adh39824 TPI promo
12	45.4	8.3	50	ADJ45801	Adj45801 TPI promo
13	45.4	8.3	50	ADL73003	Adl73003 Notch sig
14	45.4	8.3	50	ADQ14415	Adq14415 TPI promo
15	45.4	8.3	50	ADS52104	Ads52104 Notch sig
16	44	8.1	50	ACC83340	Acc83340 TPI promo
17	44	8.1	50	ACF58280	Acf58280 Oligo use
18	44	8.1	50	ADL73004	Adl73004 Notch sig

19	41.4	7.6	2000	8	ADA71938	Ada71938 Rice gene
20	41.2	7.6	1898	5	AAS85600	Aas85600 DNA encod
21	37	6.8	5791	14	ADZ64267	Adz64267 Human can
22	37	6.8	15363	14	ADZ64254	Adz64254 Human can
23	36.2	6.6	3635	6	AAL53530	Aal53530 cDNA of m
24	36.2	6.6	3635	12	ADJ75856	Adj75856 Marker ge
25	36.2	6.6	3635	14	ADZ60295	Adz60295 Murine Eh
26	36	6.6	156296	14	AE051181	Aee051181 Cancer-as
27	36	6.6	160274	14	AE051181	Aee051181 Cancer-as
28	36	6.6	160300	14	AE051181	Aee051181 Cancer-as
29	35.6	6.5	165156	13	ADZ64254	Adz64254 Human can
30	35.4	6.5	4786	4	ABL29468	Ab129468 Drosophil
31	35.2	6.5	351	6	ABL77620	Ab177620 Human ova
32	34.8	6.4	502	6	ABK62959	Abk62959 Rat seque
33	34.8	6.4	5008	4	AAH18665	Aah18665 Human cdn
34	34.8	6.4	7177	4	AAK84206	Aak84206 Human imm
35	34.8	6.4	7471	4	AAS32548	Aas32548 Human gen
36	34.8	6.4	8319	4	AAS32546	Aas32546 Human gen
37	34.8	6.4	14746	10	ADB58672	Adb58672 Toxicity-
38	34	6.2	849	10	ADC26226	Adc26226 Human NOV
39	33.8	6.2	9481	4	AAS41696	Aas41696 Genomic s
40	33.8	6.2	9481	5	ABA20646	Abaz20646 Human ner
41	33.8	6.2	100944	12	ADO59368	Ado59368 Human can
42	33.6	6.2	91823	10	ADL13497	Adl13497 Osteoarth
43	33.6	6.2	93390	10	ADD71350	Add71350 Glutamine
44	33.6	6.2	131673	12	ADQ21602	Adq21602 Human sof
45	33.4	6.1	1965	11	ACL26294	Ac126294 Rice abio

ALIGNMENTS

RESULT 1

ADO43141 ID ADO43141 standard; DNA; 545 BP.

AC ADO43141;

DT 12-AUG-2004 (first entry)

DE Epstein-Barr virus LMP2A promoter.

XX Epstein-Barr virus; LMP2A; promoter; adenovirus; vector; gene therapy;

XX cytostatic; ds.

XX Human herpesvirus 4.

XX WO2004042025-A2.

XX 21-MAY-2004.

XX 30-OCT-2003; 2003WO-US034858.

XX 01-NOV-2002; 2002US-0423203P.

XX (CELL-) CELL GENESYS INC.

XX Yu DC, Ramesh N;

XX WPI; 2004-390609/36.

XX New replication-competent adenovirus vector comprising an adenovirus gene essential for replication, useful as a vehicle for introducing new genetic capability.

XX Claim 7; SEQ ID NO 2; 36pp; English.

XX The present sequence is the Epstein-Barr virus (EBV) LMP2A gene promoter region. The LMP2 gene encodes 2 distinct proteins, LMP2A and LMP2B. LMP2A aggregates in patches within the plasma membrane of latently infected B-lymphocytes. The consistent expression of LMP2A in Hodgkin's disease and nasopharyngeal carcinoma suggests an important function for this protein in oncogenes. The invention provides replication-competent adenovirus

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OM nucleic - nucleic search, using sw model

Run on: June 6, 2006, 17:52:13 ; Search time 3685.56 Seconds
(without alignments)
8269.032 Million cell updates/sec

Title: US-10-698-160-2

Perfect score: 545

Sequence: 1 CGCACCACCTGCGCAATG.....catttcaggccggttttgca 545

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

*

EST:*

1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	13.8	587	9 DA645119	DA645119 DA645119
2	49	9.0	524	9 DA644493	DA644493 DA644493
3	44	8.1	1359	4 CA472883	CA472883 AGENCOURT
4	43.8	8.0	939	14 CNS00CNG	AL059400 Drosophil
5	42.4	7.8	823	14 AG106932	AG106932 Pan trogl
6	40.8	7.5	780	10 DT890143	DT890143 1471125 M
7	40.4	7.4	1079	12 CC268659	CC268659 CH261-97G
8	39.8	7.3	375	12 CE082035	CE082035 tigr-gss-
9	39.6	7.3	588	11 AQ531217	AQ531217 RPL11-3
10	39.4	7.2	294	4 CB852782	CB852782 UI-CF-FNO
11	39.4	7.2	650	14 AG536872	AG536872 Mus muscu
12	39.4	7.2	661	9 DR112573	DR112573 Rts1_29 D
13	39.4	7.2	692	14 CNS007WH	AL050923 Drosophil
14	39.2	7.2	405	2 BJ306689	BJ306689 BJ306689
15	39.2	7.2	1101	14 CNS016YN	AL107369 Drosophil
16	38.8	7.1	966	14 AG898391	AG898391 Oryza sat
17	38.6	7.1	784	10 DT891511	DT891511 1472661 M
18	38.4	7.0	352	11 AQ389958	AQ389958 RPL11-15
19	38	7.0	1225	14 CNS0166K	AL106358 Drosophil

C 20	37.8	6.9	401	4 BY284357	BY284357 BY284357
C 21	37.8	6.9	554	9 DN370251	DN370251 LTB3733-0
C 22	37.6	6.9	1144	12 CC258918	CC258918 CH261-164
C 23	37.4	6.9	411	4 BY424295	BY424295 BY424295
C 24	37.4	6.9	729	5 CD871322	CD871322 AZO2-117P
C 25	37.4	6.9	794	13 CW668045	CW668045 OG_BBA002
C 26	37.2	6.8	593	4 CB854072	CB854072 UI-CF-DU1
C 27	37.2	6.8	696	5 CF891453	CF891453 UI-CF-FNO
C 28	37.2	6.8	968	10 DV317960	DV317960 NABOB51TF
C 29	37	6.8	508	11 AZ007202	AZ007202 RPL1-23-3
C 30	36.8	6.8	539	9 DB333210	DB333210 DB333210
C 31	36.8	6.8	844	14 CNS0052P	AL05652 Drosophil
C 32	36.8	6.8	907	4 CB591225	CB591225 AGENCOURT
C 33	36.8	6.8	1267	12 CC260090	CC260090 CH261-165
C 34	36.6	6.7	946	14 CNS006RN	AL065838 Drosophil
C 35	36.4	6.7	588	14 CNS004M4	AL052823 Drosophil
C 36	36.4	6.7	728	14 DX304808	DX304808 OR_Aba021
C 37	36.4	6.7	1193	12 CC184353	CC184353 CH261-61H
C 38	36.2	6.6	345	4 BY293974	BY293974 BY293974
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C 42	36.2	6.6	430	4 BY288669	BY288669 BY288669
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C 44	36.2	6.6	667	7 BB641431	BB641431 BB641431
C 45	36.2	6.6	668	4 BY728949	BY728949 BY728949

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LOCUS	DA645119					587 bp mRNA clone LYMPB2002236 5', mRNA
DEFINITION	DA645119					sequence.
ACCESSION	DA645119					GI:81163469
VERSION	EST.					
KEYWORDS	Homo sapiens					(human)
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 587)					
AUTHORS	Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Iehi,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Iehibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.					
TITLE	Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes					
JOURNAL	Genome Res.	16	(1)			55-65 (2006)
PUBMED	16344560					
COMMENT	Contact: Takao Isogai FLJ Project (HRI Team) Helix Research Institute 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: flj-cdna@nifty.com					
FEATURES	NEBO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.					
source	Location/Qualifiers					
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	/mol_type="mRNA"					

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: June 6, 2006, 18:05:44 ; Search time 145.496 Seconds
(without alignments)
7008.836 Million cell updates/sec

Title: US-10-698-160-2

Perfect score: 545

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 2807332

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	36.2	6.6	3635	3 US-09-312-762A-6 Sequence 6, Appl
C 3	36	6.6	15003	3 US-09-949-016-12319 Sequence 12319, A
C 4	36	6.6	15004	3 US-09-949-016-15658 Sequence 15658, A
C 5	34.8	6.4	11366	3 US-09-949-016-13616 Sequence 13616, A
C 6	34.6	6.3	43377	3 US-09-949-016-11840 Sequence 11840, A
C 7	34.6	6.3	43378	3 US-09-949-016-11969 Sequence 11969, A
C 8	33.8	6.2	40548	3 US-09-949-016-17249 Sequence 17249, A
C 9	33.8	6.2	40547	3 US-09-949-016-13317 Sequence 13317, A
C 10	33.8	6.2	40617	3 US-09-949-016-15197 Sequence 15197, A
C 11	32.8	6.0	474	3 US-09-621-976-18033 Sequence 18033, A
C 12	32.8	6.0	24984	3 US-09-949-016-14950 Sequence 14950, A
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C 14	32.8	6.0	99304	3 US-09-949-016-15440 Sequence 15440, A
C 15	32.6	6.0	422592	3 US-09-949-016-14182 Sequence 14182, A
C 16	32.6	6.0	1185	4 US-09-297-648-4514 Sequence 4514, Ap
C 17	32.4	5.9	601	3 US-09-949-016-14470 Sequence 14470, A
C 18	32.2	5.9	11280	3 US-09-949-016-15203 Sequence 15203, A
C 19	32.2	5.9	11280	3 US-09-949-016-15203 Sequence 15204, A
C 20	32.2	5.9	43991	5 US-09-984-429-252 Sequence 252, App
C 21	32.2	5.9	44554	3 US-09-949-016-12787 Sequence 12787, A
C 22	32.2	5.9	44555	3 US-09-949-016-12043 Sequence 12043, A
C 23	32.2	5.9	199945	3 US-09-949-016-15436 Sequence 15436, A

C 24	32.2	5.9	421118	3 US-09-949-016-16297	Sequence 16297, A
C 25	32	5.9	123463	3 US-09-949-016-17078	Sequence 17078, A
C 26	32	5.9	276887	3 US-09-949-016-13840	Sequence 13840, A
C 27	31.8	5.8	601	3 US-09-949-016-54264	Sequence 54264, A
C 28	31.8	5.8	601	3 US-09-949-016-54328	Sequence 54328, A
C 29	31.6	5.8	1256	2 US-08-176-427B-9	Sequence 9, Appl
C 30	31.6	5.8	1256	2 US-08-356-060A-5	Sequence 5, Appl
C 31	31.6	5.8	1256	3 US-08-460-900C-5	Sequence 5, Appl
C 32	31.6	5.8	1256	3 US-08-674-509B-5	Sequence 5, Appl
C 33	31.6	5.8	1256	3 US-08-954-698-5	Sequence 5, Appl
C 34	31.6	5.8	1256	3 US-08-957-874-5	Sequence 5, Appl
C 35	31.6	5.8	1256	3 US-09-325-256-9	Sequence 9, Appl
C 36	31.6	5.8	1256	3 US-09-639-695-5	Sequence 5, Appl
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C 38	31.6	5.8	1256	3 US-08-954-128-5	Sequence 5, Appl
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C 44	31.6	5.8	1256	3 US-09-569-386-5	Sequence 5, Appl
C 45	31.6	5.8	1256	3 US-08-905-572A-5	Sequence 5, Appl

ALIGNMENTS

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; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:

GenCore version 5.1.1.9

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Run on: June 6, 2006, 18:14:24 ; Search time 1061.29 Seconds
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Title: US-10-698-160-2

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Scoring table:

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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7	45.4	8.3	50	9	Sequence 5, Appli
8	45.4	8.3	50	9	Sequence 34, Appl
9	45.4	8.3	50	9	Sequence 68, Appl
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11	45.4	8.3	50	10	US-10-845-834A-12
12	45.4	8.3	50	15	US-10-958-784-22
13	45.4	8.3	50	15	US-11-078-735-46
14	44	8.1	50	16	US-11-050-346-44
15	44	8.1	50	9	US-10-763-362-23
16	44	8.1	50	9	US-10-812-144-6
17	44	8.1	50	9	US-10-765-727-35
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c 19	41.2	8.1	50	16	US-11-050-346-45	Sequence 45, Appl
c 20	41.2	7.6	1898	10	US-10-450-763-21404	Sequence 21404, A
c 21	36.4	6.7	671	6	US-10-184-644-346	Sequence 346, App
c 22	36.4	6.7	671	6	US-10-184-634-346	Sequence 346, App
c 23	36.2	6.6	3635	3	US-09-312-762A-6	Sequence 6, Appli
c 24	36.2	6.6	3635	10	US-10-784-420-19	Sequence 19, Appl
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c 29	36	6.6	160300	10	US-10-893-315-151	Sequence 151, App
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ALIGNMENTS

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; Sequence 2, Application US/10698160

; Publication No. US20040171159A1

; GENERAL INFORMATION:

; APPLICANT: DC Yu

; APPLICANT: Nagarajan Ramesh

; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTOR

; FILE REFERENCE: CELL-023

; CURRENT APPLICATION NUMBER: US/10/698,160

; CURRENT FILING DATE: 2003-10-30

; PRIOR FILING DATE: 2002-11-01

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 545

; TYPE: DNA

; ORGANISM: Epstein Barr virus

US-10-698-160-2

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Best Local Similarity 100.0%; Pred. No. 2.6e-178; Mismatches 0; Indels 0; Gaps 0;

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Db 61 TGTGACCTGTCACTTCCCAAGCCCTGGCACCCTGCCAGTGCCTGGTGGAAAAATGA 120

Qy 121 CAAGGAGGAGCCCAACGGGGTTTATGTTCTCGGATACCTTTCGCAATAAAGCGCACTTGC 180

Db 121 CAAGGAGGAGCCCAACGGGGTTTATGTTCTCGGATACCTTTCGCAATAAAGCGCACTTGC 180

Qy 181 TATTTCACCTTGTGTTTGTAGTGTGGCATTGGGGGGGTGGCATTGGGGGTGGATAGCTCGCG 240

Db 181 TATTTCACCTTGTGTTTGTAGTGTGGCATTGGGGGGGTGGCATTGGGGGTGGATAGCTCGCG 240

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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1782.525 Million cell updates/sec

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Perfect score: 545
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Total number of hits satisfying chosen parameters: 493674

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	30.2	5.5	4239	6 US-10-511-937-543	Sequence 543, App
C 5	30	5.5	1370	6 US-10-953-349-34135	Sequence 34135, A
C 6	29.4	5.4	2516	6 US-10-953-349-40063	Sequence 40063, A
C 7	28.6	5.2	2448	7 US-11-217-529-3847	Sequence 3847, App
C 8	28.4	5.2	1104	6 US-10-953-349-8702	Sequence 8702, App
C 9	28.4	5.2	128361	6 US-10-505-928-151	Sequence 151, App
C 10	28.2	5.2	959	6 US-10-953-349-28855	Sequence 28855, A
C 11	28.2	5.2	1050	6 US-10-953-349-10035	Sequence 10035, A
C 12	28.2	5.2	1235	6 US-10-953-349-16861	Sequence 16861, A
C 13	28.2	5.2	1766	6 US-10-505-928-614	Sequence 614, App
C 14	28.2	5.2	2145	7 US-11-293-697-9	Sequence 9, Appli
C 15	28	5.1	849	6 US-10-953-349-34426	Sequence 34426, A
C 16	28	5.1	1706	6 US-10-505-928-762	Sequence 762, App
C 17	28	5.1	2786	6 US-10-196-749-307	Sequence 307, App
C 18	27.8	5.1	1624	6 US-10-953-349-32219	Sequence 32219, A
C 19	27.6	5.1	958	6 US-10-953-349-35887	Sequence 35887, A
C 20	27.6	5.1	3124	7 US-11-293-697-568	Sequence 568, App
C 21	27.6	5.1	3333	7 US-11-217-529-232	Sequence 232, App
C 22	27.4	5.0	584	6 US-10-488-619-1431	Sequence 1431, App
C 23	27.4	5.0	1023	7 US-11-145-307A-177	Sequence 177, App
C 24	27.4	5.0	1960	7 US-11-293-697-1665	Sequence 1665, App
C 25	27.4	5.0	2290	7 US-11-293-697-191	Sequence 191, App

ALIGNMENTS

RESULT 1

US-11-217-529-77277/c
; Sequence 77277, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77277
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77277

Query Match 5.6%; Score 30.6; DB 7; Length 666;
Best Local Similarity 58.1%; Pred. No. 0.85;
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy	74	CTTCCCAAGCCTGSCACCTGCCAGTGCCTGGTGGAGAAAATGACAAAGGAGGAGCC	133
Db	571	CTTATCATCGCTGTGTACAGGCCAAGAACTAGTTGTGCCACTTCAAAGGATGTACC	512
Qy	134	CACGGGGTTATGTTTCTGGATCTTGTGCGAA	166
Db	511	CAGTGCTTTTCAGAAGCTGTATTAAGTCCCGA	479

RESULT 2

US-11-293-697-382/c
; Sequence 382, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cdna
; FILE REFERENCE: HL-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05

Sequence 3, Appli
Sequence 155, App
Sequence 293, App
Sequence 655, App
Sequence 31, Appl
Sequence 2025, Ap
Sequence 75811, A
Sequence 1, Appli
Sequence 6, Appli
Sequence 27866, A
Sequence 1106, Ap
Sequence 517, App
Sequence 575, App
Sequence 136, App
Sequence 26032, A
Sequence 367, App
Sequence 1776, Ap
Sequence 28, Appl
Sequence 1473, Ap
Sequence 4118, Ap

26	27.4	5.0	394191	6	US-10-506-549-3
27	27.2	5.0	674	7	US-11-301-554-155
28	27.2	5.0	1173	6	US-10-953-349-293
29	27.2	5.0	3705	6	US-10-505-928-655
30	27.2	5.0	38187	6	US-10-857-260-31
31	27	5.0	891	7	US-11-217-529-2025
C 32	27	5.0	1119	7	US-11-217-529-75811
C 33	27	5.0	1719	7	US-11-269-117-1
C 34	27	5.0	8322	7	US-11-269-117-6
C 35	26.8	4.9	1459	6	US-10-953-349-27866
C 36	26.8	4.9	2442	7	US-11-293-697-1106
C 37	26.8	4.9	3690	6	US-10-196-749-517
C 38	26.8	4.9	5047	6	US-10-505-928-575
C 39	26.6	4.9	1233	7	US-11-217-529-136
C 40	26.6	4.9	1467	6	US-10-953-349-26032
C 41	26.6	4.9	1890	7	US-11-293-697-367
C 42	26.6	4.9	3194	7	US-11-293-697-1776
C 43	26.6	4.9	16009	6	US-10-857-260-28
C 44	26.4	4.8	526	7	US-11-301-554-1473
C 45	26.4	4.8	1544	6	US-10-953-349-4118

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SEARCH REQUEST FORM

Requester's Full Name: DAVID GUZO Examiner #: 70677 Date: 6/1/06
Art Unit: 1636 Phone Number: 2-0767 Serial Number: 10/698160
Location (Bldg/Room#): 2A79 (Mailbox #): 2C70 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Date: _____

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please run a regular plus interference sequence search on SEQ ID NO: 1 and 2.

1 - 575 NA
2 - 543
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